

47006

Schreiber, David

From: Fronda, Christian
Sent: Tuesday, July 17, 2001 5:32 PM
To: Schreiber, David
Subject: Protein Sequence Search on Serial No. 09/435,770

Importance: High.

Hi David, can you perform a protein sequence search on Serial No. 09/435,770 which is listed below. Thank you very much.

Christian L. Fronda
Art Unit 1652
(703)305-1252

Please perform sequence search and interference search for Serial No. 09/435,770

1. Please search SEQ ID Nos.: 1-6 against amino acid databases including pending and issued.

Please save on COMPUTER DISKETTES.

Please save results from interference searches on different diskettes from the commercial and issued search results.

Thank you very much.

Sincerely,
Chris Fronda
CM1 10B13
AU 1652
305-1252

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770B

DATE: 07/17/2001

TIME: 17:20:10

Input Set : N:\Crf3\07132001\I435770B.raw
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1 <110> APPLICANT: YAMAMOTO, Takuo
 2 MARUTA, Kazuhiko
 3 KUBOTA, Michio
 4 FUKUDA, Shigeharu
 5 MIYAKE, Toshio
 6 <120> TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,
 7 TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING
 8 SACCHARIDES USING THE ENZYMES
 9 <130> FILE REFERENCE: YAMAMOTO=16A
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/435,770B
 11 <141> CURRENT FILING DATE: 1999-11-08
 12 <150> PRIOR APPLICATION NUMBER: JP 258,394/1998
 13 <151> PRIOR FILING DATE: 1998-09-11
 14 <150> PRIOR APPLICATION NUMBER: JP 352,252/1998
 15 <151> PRIOR FILING DATE: 1998-12-11
 16 <150> PRIOR APPLICATION NUMBER: JP 16,931/1999
 17 <151> PRIOR FILING DATE: 1999-01-26
 18 <160> NUMBER OF SEQ ID NOS: 39
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 756
 23 <212> TYPE: PRT
 24 <213> ORGANISM: ARTHROBACTER sp.S34
 25 <400> SEQUENCE: 1
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 29 20 25 30
 30 Leu Tyr Leu Ser Pro Leu Leu Glu Ser Glu Ser Gly Ser His Gly
 31 35 40 45
 32 Tyr Asp Val Val Asp His Ser Arg Val Asp Ala Ala Arg Gly Gly Pro
 33 50 55 60
 34 Glu Gly Leu Ala Glu Leu Ser Arg Ala Ala His Glu Arg Gly Met Gly
 35 65 70 75 80
 36 Val Val Val Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Lys
 37 85 90 95
 38 Ala Asn Arg Trp Trp Trp Asp Val Leu Ala Arg Gly Gln Arg Ser Glu
 39 100 105 110
 40 Tyr Ala Asp Tyr Phe Asp Ile Asp Trp Glu Phe Gly Gly Arg Leu
 41 115 120 125
 42 Arg Leu Pro Val Leu Gly Asp Gly Pro Asp Glu Leu Asp Ala Leu Arg
 43 130 135 140
 44 Val Asp Gly Asp Glu Leu Val Tyr Tyr Glu His Arg Phe Pro Ile Ala
 45 145 150 155 160
 46 Glu Gly Thr Gly Gly Thr Pro Arg Glu Val His Asp Arg Gln His
 47 165 170 175
 48 Tyr Glu Leu Met Ser Trp Arg Arg Ala Asp His Asp Leu Asn Tyr Arg

Entered
PS

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53	210	215	220
54	Gly Leu Val Asp Gly Leu Arg Val Asp His Pro Asp Gly Leu Arg Ala		
55	225	230	240
56	Pro Gly Asp Tyr Leu Arg Arg Leu Ala Glu Leu Ala Gln Gly Arg Pro		
57	245	250	255
58	Ile Trp Val Glu Lys Ile Ile Glu Gly Asp Glu Arg Met Pro Pro Gln		
59	260	265	270
60	Trp Pro Ile Ala Gly Thr Thr Gly Tyr Asp Ala Leu Ala Gly Ile Asp		
61	275	280	285
62	Arg Val Leu Val Asp Pro Ala Gly Glu His Pro Leu Thr Gln Ile Val		
63	290	295	300
64	Asp Glu Ala Ala Gly Ser Pro Arg Arg Trp Ala Glu Leu Val Pro Glu		
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66	Arg Lys Arg Ala Val Ala Arg Gly Ile Leu Asn Ser Glu Ile Arg Arg		
67	325	330	335
68	Val Ala Arg Glu Leu Gly Glu Val Ala Gly Asp Val Glu Asp Ala Leu		
69	340	345	350
70	Val Glu Ile Ala Ala Leu Ser Val Tyr Arg Ser Tyr Leu Pro Phe		
71	355	360	365
72	Gly Arg Glu His Leu Asp Glu Ala Val Ala Ala Ala Gln Ala Ala Ala		
73	370	375	380
74	Pro Gln Leu Glu Ala Asp Leu Ala Ala Val Gly Ala Ala Leu Ala Asp		
75	385	390	395
76	Pro Gly Asn Pro Ala Ala Leu Arg Phe Gln Gln Thr Ser Gly Met Ile		
77	405	410	415
78	Met Ala Lys Gly Val Glu Asp Asn Ala Phe Tyr Arg Tyr Pro Arg Leu		
79	420	425	430
80	Thr Ser Leu Thr Glu Val Gly Gly Asp Pro Ser Leu Phe Ala Ile Asp		
81	435	440	445
82	Ala Ala Ala Phe His Ala Ala Gln Arg Asp Arg Ala Ala Arg Leu Pro		
83	450	455	460
84	Glu Ser Met Thr Thr Leu Thr Thr His Asp Thr Lys Arg Ser Glu Asp		
85	465	470	475
86	Thr Arg Ala Arg Ile Thr Ala Leu Ala Glu Ala Pro Glu Arg Trp Arg		
87	485	490	495
88	Arg Phe Leu Thr Glu Val Gly Gly Leu Ile Gly Thr Gly Asp Arg Val		
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90	Leu Glu Asn Leu Ile Trp Gln Ala Ile Val Gly Ala Trp Pro Ala Ser		
91	515	520	525
92	Arg Glu Arg Leu Glu Ala Tyr Ala Leu Lys Ala Ala Arg Glu Ala Gly		
93	530	535	540
94	Glu Ser Thr Asp Trp Ile Asp Gly Asp Pro Ala Phe Glu Glu Arg Leu		
95	545	550	555
96	Thr Arg Leu Val Thr Val Ala Val Glu Glu Pro Leu Val His Glu Leu		
97	565	570	575

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Input Set : N:\Crf3\07132001\I435770B.raw
Output Set: N:\CRF3\07172001\I435770B.raw

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100 Leu Ala Ala Lys Leu Leu Gln Leu Leu Ala Pro Gly Thr Pro Asp Val
101 595 600 605
102 Tyr Gln Gly Thr Glu Arg Trp Asp Arg Ser Leu Val Asp Pro Asp Asn
103 610 615 620
104 Arg Arg Pro Val Asp Phe Ala Ala Ser Glu Leu Leu Asp Arg Leu
105 625 630 635 640
106 Asp Gly Gly Trp Arg Pro Pro Val Asp Glu Thr Gly Ala Val Lys Thr
107 645 650 655
108 Leu Val Val Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu Leu
109 660 665 670
110 Phe Thr Ala Tyr His Pro Val Thr Ala Arg Gly Ala Gln Ala Glu His
111 675 680 685
112 Leu Ile Gly Phe Asp Arg Gly Gly Ala Ile Ala Leu Ala Thr Arg Leu
113 690 695 700
114 Pro Leu Gly Leu Ala Ala Gly Gly Trp Gly Asp Thr Val Val Asp
115 705 710 715 720
116 Val Gly Glu Arg Ser Leu Arg Asp Glu Leu Thr Gly Arg Glu Ala Arg
117 725 730 735
118 Gly Ala Ala Arg Val Ala Glu Leu Phe Ala Asp Tyr Pro Val Ala Leu
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120 Leu Val Glu Thr
121 755
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 6
125 <212> TYPE: PRT
126 <213> ORGANISM: ARTHROBACTER sp.S34
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129 1 5
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 6
133 <212> TYPE: PRT
134 <213> ORGANISM: ARTHROBACTER sp.S34
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136 Gly Thr Thr Gly Tyr Asp
137 1 5
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 20
141 <212> TYPE: PRT
142 <213> ORGANISM: ARTHROBACTER sp.S34
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145 1 5 10 15
146 Asp Ala Ala Arg
147 20
149 <210> SEQ ID NO: 5
150 <211> LENGTH: 20

RAW SEQUENCE LISTING

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Input Set : N:\Crf3\07132001\I435770B.raw
 Output Set: N:\CRF3\07172001\I435770B.raw

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157             20
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161 <212> TYPE: PRT
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167             20
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175     atcgtgccc acctgcacccg cctcggcgcc gactggctgt acctctcgcc gctgctcgag 120
176     tccgagtcgg gctcctcgca cggctacgac gtggtcgacc actcccgctg cgacgcccgc 180
177     cgcggcgggc cggaggggct cgccgaagctc tcccgtcggt cgcacgagcg cggcatggc 240
178     gtcgtcgctc acatcggtcc caaccacgtc ggcgtcgac cgcggaaaggc gaaccgctgg 300
179     tggtgggacg ttctggccc tggacagcg tcggagtacg ccgactactt cgacatcgac 360
180     tgggagttcg gccccggcag gctgcgcctg cccgtctcg ggcacggccc cgacgagctc 420
181     gacgcgtga gagtggatgg cgacgagctc gtctactacg agcaccgctt cccgatcgcc 480
182     gagggcaccg gccccggcac cccgcgcgag gtgcacgacc ggcagcacta cgagctgtg 540
183     tcgtggcgcc gggccgacca cgacctaacc taccgcgcgt ttttcgcgtt gaacacgctc 600
184     gcccgcgtac gctcgtgaaga cccgcgcgtt ttgcacgaca cccaccgcgat gatcgccgc 660
185     tggatcgccg agggcctcgat cgacggcctg cgcgtcgacc accccgacgg gctgcgcgc 720
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187     aagatcatcg agggcgacga gcggatgccc cgcgtcgatccatcgccg caccaccggc 840
188     tacgacgcgc tggccggat cgacggggat ctgcgtcgacc cccgcggcgat gcatccgctc 900
189     acccagatcg tcgacgaggc ggcaggcagc cccggcgat gggccgacgg gttcccgag 960
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192     gtctaccgcgat gctacccgcgat gttcggcgcc gggccgcgtt acgaaggccgtt ggcgcgcgc 1140
193     caggccgcgat ccccccgcgtt cgcgtcgcccg tccgcgcgat gctcgccgac 1200
194     cccggcaacc cccgcgcgtt cccgttcccg cagaccagcg gcatgatcgat ggccaaggcc 1260
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Input Set : N:\CrF3\07132001\I435770B.raw
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 203 gtcgacgagc tgacggccgc cgggtactcc aacggcctcg cggcgaagct gctgcagctg 1800
 204 ctcgcccccg gaacccccga cgtgtaccag ggcacccaac gctgggaccg gtcgctggtg 1860
 205 gacccggaca accgtcgccc cgtggatttc gccgcccgc cat ccgagctgct cgaccgcctc 1920
 206 gacggcggct ggcggccgc cgtcgacgag accggcgcgg tcaagacgct cgtcgctcc 1980
 207 cgcgcgctgc ggctgcgcgc cgaccggccc gagctttca ccgcgtacca cccggtcacg 2040
 208 ggcgcgcgcg cgcaggccga gcacctgatc ggcttcgacc gccggccgcgc gatcgccctg 2100
 209 gccacccgcgc tgccgctcgcc ctcgcgcgc gcaggcggct ggggcgacac ggtcgctgac 2160
 210 gtcggcgagc ggagcctgcg cgacgagctg accggccgcg aggcccgcgg agcggcgcgc 2220
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213 <210> SEQ ID NO: 8
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 215 <212> TYPE: DNA
 216 <213> ORGANISM: ARTHROBACTER sp.S34
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 220 <210> SEQ ID NO: 9
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 222 <212> TYPE: PRT
 223 <213> ORGANISM: ARTHROBACTER sp.S34
 224 <400> SEQUENCE: 9
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 227 Asn Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu
 35 40 45
 228 Val Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro
 50 55 60
 229 Arg Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe
 65 70 75 80
 230 Asp Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp
 85 90 95
 231 Leu Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro
 100 105 110
 232 Glu Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg
 115 120 125
 233 Leu Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly
 130 135 140
 234 Thr His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu
 145 150 155 160
 235 Pro Tyr Gly Gly Pro Glu Ala Tyr Gln Arg Phe Val Asp Ala Cys His
 165 170 175
 236 Ala Arg Gly Leu Ala Val Val Gln Asp Val Val Tyr Asn His Leu Gly
 180 185 190
 237 Pro Ser Gly Asn His Leu Pro Asp Phe Gly Pro Tyr Leu Gly Ser Gly
 195 200 205
 238 Ala Ala Asn Thr Trp Gly Asp Ala Leu Asn Leu Asp Gly Pro Leu Ser
 210 215 220

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/435,770B

DATE: 07/17/2001

TIME: 17:20:11

Input Set : N:\Crf3\07132001\I435770B.raw
Output Set: N:\CRF3\07172001\I435770B.raw

L:10 M:270 C: Current Application Number differs, Wrong Format

L:681 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31

L:684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31